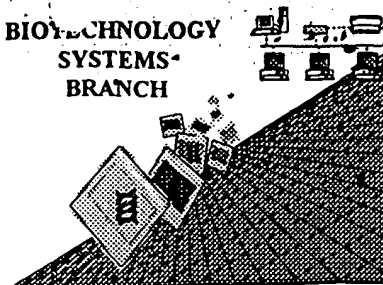


## RAW SEQUENCE LISTING ERROR REPORT

BIO TECHNOLOGY  
SYSTEMS-  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/763129

Source: PCT

Date Processed by STIC: 08/30/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/763129

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11   ✓   Use of <220>      Sequence(s) 668 missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

## RAW SEQUENCE LISTING

DATE: 08/30/2001

PATENT APPLICATION: US/09/763,129

TIME: 06:16:21

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

```

3 <110> APPLICANT: CO, MAN SUNG
4   VASQUEZ, MAXIMILIANO
6 <120> TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
FACTOR MONOCLONAL
7   ANTIBODY
9 <130> FILE REFERENCE: 202617US0PCT
11 <140> CURRENT APPLICATION NUMBER: 09/763,129
C--> 12 <141> CURRENT FILING DATE: 2001-05-16
14 <150> PRIOR APPLICATION NUMBER: PCT/US99/16724
15 <151> PRIOR FILING DATE: 1999-08-19
17 <150> PRIOR APPLICATION NUMBER: 09/136,315
18 <151> PRIOR FILING DATE: 1998-08-19
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 417
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(417)
32 <223> OTHER INFORMATION:
35 <400> SEQUENCE: 1
36 atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc      48
37 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
38 1           5           10           15
40 cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act      96
41 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
42           20           25           30
44 gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt      144
45 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
46           35           40           45
48 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa      192
49 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50           50           55           60
52 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca      240
53 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
54 65           70           75           80
56 tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg      288
57 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
58           85           90           95
60 ctg tac ctg caa atg agt caa gtg aga tct gag gac aca gcc ctt tac      336
61 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
62           100          105          110
64 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac      384
65 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
66           115          120          125
68 tgg ggc caa ggg act ctg gtc tct gtc tcg cca      417

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,129

DATE: 08/30/2001

TIME: 06:16:21

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

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69 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
70      130                      135
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 139
75 <212> TYPE: PRT
76 <213> ORGANISM: Mus musculus
78 <400> SEQUENCE: 2
80 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
81 1      5      10      15
84 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
85      20      25      30
88 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
89      35      40      45
92 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
93      50      55      60
96 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
97 65      70      75      80
100 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
101      85      90      95
104 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
105      100     105     110
108 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
109      115     120     125
112 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
113      130                      135
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 381
118 <212> TYPE: DNA
119 <213> ORGANISM: Mus musculus
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (1)..(381)
124 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 3
128 atg agt gtg ccc act cag gtc ctg ggg ttg ctg ctg ctg tgg ctt aca      48
129 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Trp Leu Thr
130 1      5      10      15
132 gat gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct      96
133 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
134      20      25      30
136 gta tct gtg gga gaa act gtc acc atc aca tgt cga gca agt gag aat      144
137 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
138      35      40      45
140 att tac aat aat tta gct tgg tat cag cag aga cag gga aaa tct cct      192
141 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
142      50      55      60
144 cag ctc ctg gtc tat gct gca aca aac tta gca gat ggt gtg cca tca      240
145 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
146 65      70      75      80

```

## RAW SEQUENCE LISTING

DATE: 08/30/2001

PATENT APPLICATION: US/09/763,129

TIME: 06:16:21

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

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148 agg ttc agt ggc agt gga tca ggc aca cag tat tcc ctc aag atc gac      288
149 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
150                               85                               90                               95
152 agc ctg cag tct gaa gat ttt ggg agt tat tac tgt caa cat ttg tgg      336
153 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
154                               100                               105                               110
156 act tct ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa      381
157 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
158                               115                               120                               125
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 127
163 <212> TYPE: PRT
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 4
168 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
169 1                               5                               10                               15
172 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
173                               20                               25                               30
176 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
177                               35                               40                               45
180 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
181                               50                               55                               60
184 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
185 65                               70                               75                               80
188 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
189                               85                               90                               95
192 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
193                               100                               105                               110
196 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
197                               115                               120                               125
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 417
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Synthetic DNA
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)..(417)
211 <223> OTHER INFORMATION:
214 <400> SEQUENCE: 5
215 atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc      48
216 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
217 1                               5                               10                               15
219 cag tgt gag gtg caa ctt gtc gag tct gga ggt gga cta gtg cag cct      96
220 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
221                               20                               25                               30
223 gga gga tca ctg aga ctc tcc tgt gca gcc tca gga ttc gat ttt agt      144
224 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser

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## RAW SEQUENCE LISTING

DATE: 08/30/2001

PATENT APPLICATION: US/09/763,129

TIME: 06:16:21

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

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225          35          40          45
227 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag      192
228 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
229          50          55          60
231 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca      240
232 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
233 65          70          75          80
235 tct cta aag gat aaa ttc acc atc tcc aga gac aac gcc aaa aat acg      288
236 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
237          85          90          95
239 ctg tac ctg caa atg aac tca ttg aga gct gag gac acg gcc gtt tac      336
240 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
241          100          105          110
243 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac      384
244 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
245          115          120          125
247 tgg ggc caa ggg act ctg gtc acc gtc tcc tca      417
248 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
249          130          135

```

252 <210> SEQ ID NO: 6 *Errored: An explanation or description of your artificial protein sequence is required in field 223.*

253 <211> LENGTH: 139

254 <212> TYPE: PRT

255 <213> ORGANISM: Artificial Sequence

257 <220> FEATURE:

258 <223> OTHER INFORMATION: Synthetic DNA

260 <400> SEQUENCE: 6

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262 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
263 1          5          10          15
266 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
267          20          25          30
270 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
271          35          40          45
274 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
275          50          55          60
278 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
279 65          70          75          80
282 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
283          85          90          95
286 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
287          100          105          110
290 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
291          115          120          125
294 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
295          130          135
298 <210> SEQ ID NO: 7
299 <211> LENGTH: 381
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:

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The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 08/30/2001

PATENT APPLICATION: US/09/763,129

TIME: 06:16:21

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

304 &lt;223&gt; OTHER INFORMATION: Synthetic DNA

306 &lt;220&gt; FEATURE:

307 &lt;221&gt; NAME/KEY: CDS.

308 &lt;222&gt; LOCATION: (1)..(381)

309 &lt;223&gt; OTHER INFORMATION:

312 &lt;400&gt; SEQUENCE: 7

313 atg agt gtg ccc act cag gtc ctg ggg ttg ctg ctg ctg tgg ctt aca 48

314 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr

315 1 5 10 15

317 gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct 96

318 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser

319 20 25 30

321 gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat 144

322 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn

323 35 40 45

325 att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct 192

326 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro

327 50 55 60

329 aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca 240

330 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser

331 65 70 75 80

333 agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc 288

334 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser

335 85 90 95

337 agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg 336

338 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp

339 100 105 110

341 act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa 381

342 Thr Ser Pro Tyr Thr Phe Gly Gly Thr Lys Val Glu Ile Lys

343 115 120 125

346 &lt;210&gt; SEQ ID NO: 8

347 &lt;211&gt; LENGTH: 127

348 &lt;212&gt; TYPE: PRT

349 &lt;213&gt; ORGANISM: Artificial Sequence

351 &lt;220&gt; FEATURE:

352 &lt;223&gt; OTHER INFORMATION: Synthetic DNA

354 &lt;400&gt; SEQUENCE: 8

356 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr

357 1 5 10 15

360 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser

361 20 25 30

364 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn

365 35 40 45

368 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro

369 50 55 60

372 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser

373 65 70 75 80

376 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser

377 85 90 95

Errored: A description of your artificial protein sequence  
is ~~not~~ required in field 223.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/763,129

DATE: 08/30/2001

TIME: 06:16:22

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\I763129.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date